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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/852,261

DATE: 10/23/2001

TIME: 16:03:01

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Output Set: N:\CRF3\10232001\I852261.raw

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3 <110> APPLICANT: GOLDSPIK, GEOFFREY
4   TERENGHI, GIORGIO
6 <120> TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
8 <130> FILE REFERENCE: 117-351
10 <140> CURRENT APPLICATION NUMBER: 09/852,261
11 <141> CURRENT FILING DATE: 2001-05-10
13 <150> PRIOR APPLICATION NUMBER: GB 0011278.9
14 <151> PRIOR FILING DATE: 2000-05-10
16 <160> NUMBER OF SEQ ID NOS: 14
18 <170> SOFTWARE: PatentIn Ver. 2.1
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21 <211> LENGTH: 517
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
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27 agggggtttt atttcaacaa gcccacaggg tatggctcca gcagtcggag ggcgcctcag 120
28 acaggcatcg tggatgagtg ctgcttccgg agctgtgata taaggaggct ggagatgtat 180
29 tgcgcacccc tcaagcctgc caagtcagct cgctctgtcc gtgcccagcg ccacaccgac 240
30 atgcccaaga cccagaagta tcagccccca tctaccaaca agaacacgaa gtctcagaga 300
31 aggaaaggaa gtacatttga agaacacaag tagagggagt gcaggaaaca agaactacag 360
32 gatgtagaag acccttctga ggagtgaaga aggacaggcc accgcaggac cctttgctct 420
33 gcacagttac ctgtaaacad tggaataccg gccaaaaaat aagtttgatc acatttcaaa 480
34 gatggcattt cccccaatga aatacacaag taaacat 517
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38 <211> LENGTH: 110
39 <212> TYPE: PRT
40 <213> ORGANISM: Homo sapiens
42 <400> SEQUENCE: 2
43 Gly Pro Glu Thr Leu Cys Gly Ala Glu Leu Val Asp Ala Leu Gln Phe
44   1           5           10           15
46 Val Cys Gly Asp Arg Gly Phe Tyr Phe Asn Lys Pro Thr Gly Tyr Gly
47   20           25           30
49 Ser Ser Ser Arg Arg Ala Pro Gln Thr Gly Ile Val Asp Glu Cys Cys
50   35           40           45
52 Phe Arg Ser Cys Asp Leu Arg Arg Leu Glu Met Tyr Cys Ala Pro Leu
53   50           55           60
55 Lys Pro Ala Lys Ser Ala Arg Ser Val Arg Ala Gln Arg His Thr Asp
56   65           70           75           80
58 Met Pro Lys Thr Gln Lys Tyr Gln Pro Pro Ser Thr Asn Lys Asn Thr
59   85           90           95
61 Lys Ser Gln Arg Arg Lys Gly Ser Thr Phe Glu Glu His Lys
62   100          105          110
65 <210> SEQ ID NO: 3
66 <211> LENGTH: 539
67 <212> TYPE: DNA
68 <213> ORGANISM: Rattus sp.

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70 &lt;400&gt; SEQUENCE: 3

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71 ggaccagaga ccctttgcgg ggctgagctg gtggacgctc ttcagttcgt gtgtggacca 60
72 aggggctttt acttcaacaa gccacagtc tatggctcca gcattcggag ggcaccacag 120
73 acgggcattg tggatgagtg ttgcttcgg agctgtgatc tgaggaggct ggagatgtac 180
74 tgtgtccgct gcaagcctac aaagtcagct cgttccatcc gggcccagcg ccacactgac 240
75 atgcccaga ctcagaagtc ccagccccta tcgacacaca agaaaaggaa gctgcaaagg 300
76 agaaggaaag gaagtacact tgaagaacac aagtagagga agtgcaggaa acaagacct 360
77 cagaatgtag gaggagcctc ccgaggaaca gaaaatgcca cgtcacgcga agatcctttg 420
78 ctgcttgagc aacctgcaaa acatcggaac acctgccaaa tatcaataat gagttcaata 480
79 tcatttcaga gatgggcatt tccctcaatg aaatacaca gtaaaccatt ccggaattc 539

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82 &lt;210&gt; SEQ ID NO: 4

83 &lt;211&gt; LENGTH: 111

84 &lt;212&gt; TYPE: PRT

85 &lt;213&gt; ORGANISM: Rattus sp.

87 &lt;400&gt; SEQUENCE: 4

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88 Gly Pro Glu Thr Leu Cys Gly Ala Glu Leu Val Asp Ala Leu Gln Phe
89   1           5           10           15
91 Val Cys Gly Pro Arg Gly Phe Tyr Phe Asn Lys Pro Thr Val Tyr Gly
92           20           25           30
94 Ser Ser Ile Arg Arg Ala Pro Gln Thr Gly Ile Val Asp Glu Cys Cys
95           35           40           45
97 Phe Arg Ser Cys Asp Leu Arg Arg Leu Glu Met Tyr Cys Val Arg Cys
98           50           55           60
100 Lys Pro Thr Lys Ser Ala Arg Ser Ile Arg Ala Gln Arg His Thr Asp
101  65           70           75           80
103 Met Pro Lys Thr Gln Lys Ser Gln Pro Leu Ser Thr His Lys Lys Arg
104           85           90           95
106 Lys Leu Gln Arg Arg Lys Gly Ser Thr Leu Glu Glu His Lys
107           100          105          110

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110 &lt;210&gt; SEQ ID NO: 5

111 &lt;211&gt; LENGTH: 523

112 &lt;212&gt; TYPE: DNA

113 &lt;213&gt; ORGANISM: Oryctolagus cuniculus

115 &lt;400&gt; SEQUENCE: 5

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116 ggaccggaga cgctctgcgg tgctgagctg gtggatgctc ttcagttcgt gtgtggagac 60
117 aggggctttt atttcaacaa gccacagga tacggctcca gcagtcggag ggcacctcag 120
118 acaggcatcg tggatgagtg ctgcttcgg agctgtgatc tgaggaggct ggagatgtac 180
119 tgtgcacccc tcaagccggc aaaggcagcc cgctccgtcc gtgcccagcg ccacaccgac 240
120 atgcccaga ctcagaagta tcagcctcca tctaccaaca agaaaatgaa gtctcagagg 300
121 agaaggaaag gaagtacatt tgaagaacac aagtagaggg agtgcaggaa acaagaacta 360
122 caggatgtag gaagaccctt ctgaggagtg aagaaggaca ggccaccgca ggaccctttg 420
123 ctctgcacag ttacctgtaa acattggaat accggccaaa aaataagttt gatcacattt 480
124 caaagatggc atttccccca atgaaataca caagtaaaca ttc 523

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127 &lt;210&gt; SEQ ID NO: 6

128 &lt;211&gt; LENGTH: 111

129 &lt;212&gt; TYPE: PRT

130 &lt;213&gt; ORGANISM: Oryctolagus cuniculus

132 &lt;400&gt; SEQUENCE: 6

133 Gly Pro Glu Thr Leu Cys Gly Ala Glu Leu Val Asp Ala Leu Gln Phe

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134      1              5              10              15
136 Val Cys Gly Asp Arg Gly Phe Tyr Phe Asn Lys Pro Thr Gly Tyr Gly
137              20              25              30
139 Ser Ser Ser Arg Arg Ala Pro Gln Thr Gly Ile Val Asp Glu Cys Cys
140              35              40              45
142 Phe Arg Ser Cys Asp Leu Arg Arg Leu Glu Met Tyr Cys Ala Pro Leu
143              50              55              60
145 Lys Pro Ala Lys Ala Ala Arg Ser Val Arg Ala Gln Arg His Thr Asp
146      65              70              75              80
148 Met Pro Lys Thr Gln Lys Tyr Gln Pro Pro Ser Thr Asn Lys Lys Met
149              85              90              95
151 Lys Ser Gln Arg Arg Arg Lys Gly Ser Thr Phe Glu Glu His Lys
152              100              105              110
155 <210> SEQ ID NO: 7
156 <211> LENGTH: 10
157 <212> TYPE: DNA
158 <213> ORGANISM: Artificial Sequence
160 <220> FEATURE:
161 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
162     oligonucleotide
164 <400> SEQUENCE: 7
165 gccaccatgg                                     10
168 <210> SEQ ID NO: 8
169 <211> LENGTH: 10
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
175     oligonucleotide
177 <400> SEQUENCE: 8
178 gcccccatgg                                     10
181 <210> SEQ ID NO: 9
182 <211> LENGTH: 318
183 <212> TYPE: DNA
184 <213> ORGANISM: Homo sapiens
186 <400> SEQUENCE: 9
187 ggaccggaga cgctctgagg ggctgagctg gtggatgctc ttcagttcgt gtgtggagac 60
188 aggggctttt atttcaacaa gcccacaggg tatggctcca gcagtcggag ggcgcctcag 120
189 acaggcatcg tggatgagtg ctgcttcagg agctgtgatc taaggaggct ggagatgtat 180
190 tgcgcacccc tcaagcctgc caagtcagct cgctctgtcc gtgcccagcg ccacaccgac 240
191 atgccaaga cccagaagga agtacatttg aagaacgcaa gtagaggagg tgcaggaaac 300
192 aagaactaca ggatgtag                                     318
195 <210> SEQ ID NO: 10
196 <211> LENGTH: 105
197 <212> TYPE: PRT
198 <213> ORGANISM: Homo sapiens
200 <400> SEQUENCE: 10
201 Gly Pro Glu Thr Leu Cys Gly Ala Glu Leu Val Asp Ala Leu Gln Phe
202      1              5              10              15

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204 Val Cys Gly Asp Arg Gly Phe Tyr Phe Asn Lys Pro Thr Gly Tyr Gly
205          20          25          30
207 Ser Ser Ser Arg Arg Ala Pro Gln Thr Gly Ile Val Asp Glu Cys Cys
208          35          40          45
210 Phe Arg Ser Cys Asp Leu Arg Arg Leu Glu Met Tyr Cys Ala Pro Leu
211          50          55          60
213 Lys Pro Ala Lys Ser Ala Arg Ser Val Arg Ala Gln Arg His Thr Asp
214          65          70          75          80
216 Met Pro Lys Thr Gln Lys Glu Val His Leu Lys Asn Ala Ser Arg Gly
217          85          90          95
219 Ser Ala Gly Asn Lys Asn Tyr Arg Met
220          100          105
223 <210> SEQ ID NO: 11
224 <211> LENGTH: 487
225 <212> TYPE: DNA
226 <213> ORGANISM: Rattus sp.
228 <400> SEQUENCE: 11
229 ggaccagaga ccctttgcgg ggctgagctg gtggacgctc ttcagttcgt gtgtggacca 60
230 aggggctttt acttcaacaa gccacagtc tatggctcca gcattcggag ggcaccacag 120
231 acgggcattg tggatgagtg ttgcttcgg agctgtgatc tgaggaggct ggagatgtac 180
232 tgtgtccgct gcaagcctac aaagtcagct cgttccatcc gggcccagcg ccacactgac 240
233 atgcccaga ctcagaagga agtacacttg aagaacacaa gtagaggaag tgcaggaaac 300
234 aagacctaca gaatgtagga ggagcctccc gaggaacaga aaatgccacg tcaccgcaag 360
235 atcctttgct gcttgagcaa cctgcaaaac atcggaacac ctgccaata tcaataatga 420
236 gttcaatatc atttcagaga tgggcatttc cctcaatgaa atacacaagt aaacattccc 480
237 ggaattc 487
240 <210> SEQ ID NO: 12
241 <211> LENGTH: 105
242 <212> TYPE: PRT
243 <213> ORGANISM: Rattus sp.
245 <400> SEQUENCE: 12
246 Gly Pro Glu Thr Leu Cys Gly Ala Glu Leu Val Asp Ala Leu Gln Phe
247 1 5 10 15
249 Val Cys Gly Pro Arg Gly Phe Tyr Phe Asn Lys Pro Thr Val Tyr Gly
250 20 25 30
252 Ser Ser Ile Arg Arg Ala Pro Gln Thr Gly Ile Val Asp Glu Cys Cys
253 35 40 45
255 Phe Arg Ser Cys Asp Leu Arg Arg Leu Glu Met Tyr Cys Val Arg Cys
256 50 55 60
258 Lys Pro Thr Lys Ser Ala Arg Ser Ile Arg Ala Gln Arg His Thr Asp
259 65 70 75 80
261 Met Pro Lys Thr Gln Lys Glu Val His Leu Lys Asn Thr Ser Arg Gly
262 85 90 95
264 Ser Ala Gly Asn Lys Thr Tyr Arg Met
265 100 105
268 <210> SEQ ID NO: 13
269 <211> LENGTH: 471
270 <212> TYPE: DNA
271 <213> ORGANISM: Oryctolagus cuniculus

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273 &lt;400&gt; SEQUENCE: 13

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274 ggaccggaga cgctctgagg tgctgagctg gtggatgctc ttcagttcgt gtgtggagac 60
275 aggggctttt atttcaacaa gcccacagga tacggctcca gcagtcggag ggcacctcag 120
276 acaggcatcg tggatgagtg ctgcttccgg agctgtgatc tgaggaggct ggagatgtac 180
277 tgtgcacccc tcaagccggc aaaggcagcc cgctccgtcc gtgcccagcg ccacaccgac 240
278 atgcccaga ctcagaagga agtacatttg aagaacacaa gtagagggag tgcaggaaac 300
279 aagaactaca ggatgtagga agacccttct gaggagtga gaaggacagg ccaccgcagg 360
280 accctttgct ctgcacagtt acctgtaaac attggaatac cggccaaaaa ataagtttga 420
281 tcacatttca aagatggcat ttccccaat gaaatacaca agtaaacatt c 471

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284 &lt;210&gt; SEQ ID NO: 14

285 &lt;211&gt; LENGTH: 105

286 &lt;212&gt; TYPE: PRT

287 <213> ORGANISM: *Oryctolagus cuniculus*

289 &lt;400&gt; SEQUENCE: 14

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290 Gly Pro Glu Thr Leu Cys Gly Ala Glu Leu Val Asp Ala Leu Gln Phe
291   1           5           10           15
293 Val Cys Gly Asp Arg Gly Phe Tyr Phe Asn Lys Pro Thr Gly Tyr Gly
294           20           25           30
296 Ser Ser Ser Arg Arg Ala Pro Gln Thr Gly Ile Val Asp Glu Cys Cys
297           35           40           45
299 Phe Arg Ser Cys Asp Leu Arg Arg Leu Glu Met Tyr Cys Ala Pro Leu
300           50           55           60
302 Lys Pro Ala Lys Ala Ala Arg Ser Val Arg Ala Gln Arg His Thr Asp
303  65           70           75           80
305 Met Pro Lys Thr Gln Lys Glu Val His Leu Lys Asn Thr Ser Arg Gly
306           85           90           95
308 Ser Ala Gly Asn Lys Asn Tyr Arg Met
309           100          105

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/852,261

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